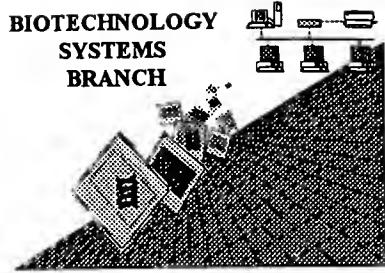


*re-rer* F. Hammond

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:**

Application Serial Number: 09/265,540

Art Unit / Team No.: 1600

Date Processed by STIC: 3/24/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**MARK SPENCER 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED   SUGGESTED CORRECTION

SERIAL NUMBER: 09/265,540

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1  Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.  
All text must be visible on page.

4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length Sequence(s)  contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) features section that some may be missing.

7  Wrong Designation Sequence(s)  contain amino acid or nucleic acid designators which are not standard representations as per the Sequence Rules (Please refer to paragraph 1.822)

8  Skipped Sequences (OLD RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence:  
**(2) INFORMATION FOR SEQ ID NO:X:**  
**(i) SEQUENCE CHARACTERISTICS:**(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
**(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:**  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES) Sequence(s)  missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence Id number  
<400> sequence Id number  
000

10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11  Use of <213>Organism (NEW RULES) Sequence(s)  are missing this mandatory field or its response.

12  Use of <220>Feature (NEW RULES) Sequence(s)  are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)  
(Sec. 1.823 of new Sequence Rules)

13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

DATE: 03/24/1991  
TIME: 16:28:51

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/265,540

Input Set: I265540.RAW

This Raw Listing contains the General Information Section and up to first 5 pages.

1 <110> APPLICANT: Parham, Christi L. Does Not Comply  
2 Moore, Kevin W. Corrected Diskette Needed  
3 Murgolo, Nicholas J.  
4 Bazan, J. Fernando  
5 <120> TITLE OF INVENTION: Human Receptor Proteins; Related Reagents and Methods  
6 <130> FILE REFERENCE: DX0804  
7 <140> CURRENT APPLICATION NUMBER: US/09/265,540  
8 <141> CURRENT FILING DATE: 1999-03-08  
9 <160> NUMBER OF SEQ ID NOS: 6  
10 <170> SOFTWARE: PatentIn Ver. 2.0  
11 <210> SEQ ID NO 1  
12 <211> LENGTH: 1381  
13 <212> TYPE: DNA  
14 <213> ORGANISM: primate  
15 <220> FEATURE:  
16 <221> NAME/KEY: CDS  
17 <222> LOCATION: (132)..(1064)  
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20 agatggctga gatggacaga atgctttatt ttggaaagaa acaatgttct aggtcaaact 120  
21 gaggctacca a atg cag act ttc aca atg gtt cta gaa gaa atc tgg aca 170  
22 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr  
23 1 5 10  
24 agt ctt ttc atg tgg ttt ttc tac gca ttg att cca tgt ttg ctc aca 218  
25 Ser Leu Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr  
26 15 20 25  
27 gat gaa gtg gcc att ctg cct gcc cct cag aac ctc tct gta ctc tca 266  
28 Asp Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
29 30 35 40 45  
30 acc aac atg aag cat ctc ttg atg tgg agc cca gtg atc gcg cct gga 314  
31 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly  
32 50 55 60  
33 gaa aca gtg tac tat tct gtc gaa tac cag ggg gag tac gag agc ctg 362  
34 Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu Ser Leu  
35 65 70 75  
36 tac acg agc cac atc tgg atc ccc agc agc tgg tgc tca ctc act gaa 410  
37 Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu  
38 80 85 90  
39 ggt cct gag tgt gat gtc act gat gac atc acg gcc act gtg cca tac 458  
40 Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr  
41 95 100 105  
42 aac ctt cgt gtc agg gcc aca ttg ggc tca cag acc tca gcc tgg agc 506  
43 Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser  
44 110 115 120 125

*PL 2/31*

PAGE: 2

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/265,540DATE: 03/24/1995  
TIME: 16:28:51

Input Set: I265540.RAW

45 atc ctg aag cat ccc ttt aat aga aac tca acc atc ctt acc cga cct 554  
 46 Ile Leu Lys His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro  
 47 130 135 140  
 W--> 48 *see item 10* ggg atg gag atc acc aaa at ggc ttc cac ctg gtt att gag ctg gag 602  
 49 Gly Met Glu Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu  
 50 145 150 155  
 51 *or* gac ctg ggg ccc cag ttt gag ttc ctt gtg gcc tac tgg asg agg gag 650  
 52 *Envr* Asp Leu Gly Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu  
 53 160 165 170  
 54 *summary* cct ggt gcc gag gaa cat gtc aaa atg gtg agg agt ggg ggt att cca 698  
 55 *sheet* Pro Gly Ala Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro  
 56 175 180 185  
 57 gtg cac cta gaa acc atg gag cca ggg gct gca tac tgt gtg aag gcc 746  
 58 Val His Leu Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala  
 59 190 195 200 205  
 60 cag aca ttc gtg aag gcc att ggg arg tac agc gcc ttc agc cag aca 794  
 61 Gln Thr Phe Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr  
 62 210 215 220  
 63 gaa tgt gtg gar gtg caa gga gag gcc att ccc ctg gta ctg gcc ctg 842  
 64 Glu Cys Val Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu  
 65 225 230 235  
 66 ttt gcc ttt gtt ggc ttc atg ctg atc ctt gtg gtc cca ctg ttc 890  
 67 Phe Ala Phe Val Gly Phe Met Leu Ile Leu Val Val Pro Leu Phe  
 68 240 245 250  
 69 gtc tgg aaa atg ggc cgg ctg ctc cag tac tcc tgt tgc ccc gtg gtg 938  
 70 Val Trp Lys Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val  
 71 255 260 265  
 72 gtc ctc cca gac acc ttg aaa ata acc aat tca ccc cag aag tta atc 986  
 73 Val Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile  
 74 270 275 280 285  
 75 agc tgc aga agg gag gag gtg gat gcc tgt gcc acg gct gtg atg tct 1034  
 76 Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser  
 77 290 295 300  
 78 cct gag gaa ctc ctc agg gcc tgg atc tca taggtttgcg gaagggccca 1084  
 79 Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser  
 80 305 310  
 81 ggtgaagccg agaacctggc ctgcattgaca tggaaaccat gaggggacaa gttgtgtttc 1144  
 82 tgggttccgc cacggacaag ggtatgagaga agtaggaaga gcctgttgc tacaagtcta 1204  
 83 gaagcaacca tcagaggcag ggtgggttgc ckaacagaac aaytgactga ggytakrggg 1264  
 84 gwtgtgaccc ttagactktg ggstkscayt tgcwtgggtg agcaaccctg ggaaaagtga 1324  
 85 cttcatccct tnggtccnaa gtttctcat ctgtaatggg gatncctac aaaactg 1381  
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 88 <212> TYPE: PRT  
 89 <213> ORGANISM: primate  
 90 <400> SEQUENCE: 2  
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 92 1 5 10 15  
 93 Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp Glu Val  
 94 20 25 30

PAGE: 3

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/265,540DATE: 03/24/1991  
TIME: 16:28:51

Input Set: I265540.RAW

95 Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser Thr Asn Met  
 96 35 40 45  
 97 Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro Gly Glu Thr Val  
 98 50 55 60  
 99 Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Ser Leu Tyr Thr Ser  
 100 65 70 75 80  
 101 His Ile Trp Ile Pro Ser Ser Trp Cys Ser Leu Thr Glu Gly Pro Glu  
 102 85 90 95  
 103 Cys Asp Val Thr Asp Asp Ile Thr Ala Thr Val Pro Tyr Asn Leu Arg  
 104 100 105 110  
 105 Val Arg Ala Thr Leu Gly Ser Gln Thr Ser Ala Trp Ser Ile Leu Lys  
 106 115 120 125  
 107 His Pro Phe Asn Arg Asn Ser Thr Ile Leu Thr Arg Pro Gly Met Glu  
 108 130 135 140  
 109 Ile Xaa Lys Xaa Gly Phe His Leu Val Ile Glu Leu Glu Asp Leu Gly  
 110 145 150 155 160  
 111 Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp Xaa Arg Glu Pro Gly Ala  
 112 165 170 175  
 113 Glu Glu His Val Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu  
 114 180 185 190  
 115 Glu Thr Met Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe  
 116 195 200 205  
 117 Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val  
 118 210 215 220  
 119 Xaa Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe  
 120 225 230 235 240  
 121 Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp Lys  
 122 245 250 255  
 123 Met Gly Arg Leu Leu Gln Tyr Ser Cys Cys Pro Val Val Val Leu Pro  
 124 260 265 270  
 125 Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile Ser Cys Arg  
 126 275 280 285  
 127 Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met Ser Pro Glu Glu  
 128 290 295 300  
 129 Leu Leu Arg Ala Trp Ile Ser  
 130 305 310  
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 132 <211> LENGTH: 1244  
 133 <212> TYPE: DNA  
 134 <213> ORGANISM: primate  
 135 <220> FEATURE:  
 136 <221> NAME/KEY: CDS  
 137 <222> LOCATION: (2)..(694)  
 138 <400> SEQUENCE: 3  
 139 c cgg gtc gac cca cgc gtc cgc ctg gtt tcc ccc tgg ctg aca gtg cct 49  
 140 Arg Val Asp Pro Arg Val Arg Leu Val Ser Pro Trp Leu Thr Val Pro  
 141 1 5 10 15  
 142 tgg ttc ctg tcc tgt tgg aat gtt acc att ggg cct cct gag agc atc 97  
 143 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 144 20 25 30

PAGE: 4

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/265,540DATE: 03/24/1999  
TIME: 16:28:51

Input Set: I265540.RAW

145	tgg	gtg	acg	ccg	gga	gaa	gcc	tcc	ctc	atc	atc	agg	ttc	tcc	tct	ccc	145
146	Trp	Val	Thr	Pro	Gly	Glu	Ala	Ser	Leu	Ile	Ile	Arg	Phe	Ser	Ser	Pro	
147	35								40					45			
148	ttc	gac	gtc	cct	ccc	aac	ctg	ggc	tat	ttc	cag	tac	tat	gtc	cat	tay	193
149	Phe	Asp	Val	Pro	Pro	Asn	Leu	Gly	Tyr	Phe	Gln	Tyr	Tyr	Val	His	Xaa	
150	50								55					60			
151	tgg	gaa	aag	gcf	gga	atc	caa	aag	gtt	aaa	ggf	cct	ttc	aag	agc	aac	241
152	Trp	Glu	Lys	Ala	Gly	Ile	Gln	Lys	Val	Lys	Gly	Pro	Phe	Lys	Ser	Asn	
153	65								70					75			80
154	tcc	atc	gtg	ttg	gat	ggc	ttg	aga	ccc	tta	aga	gaa	tac	tgt	tta	caa	289
155	Ser	Ile	Val	Leu	Asp	Gly	Leu	Arg	Pro	Leu	Arg	Glu	Tyr	Cys	Leu	Gln	
156	85								90					95			
157	gtg	aag	gcf	cat	ctc	ttt	cgc	aca	tcc	tgc	aac	acc	tct	agg	ccc	ggc	337
158	Val	Lys	Ala	His	Leu	Phe	Arg	Thr	Ser	Cys	Asn	Thr	Ser	Arg	Pro	Gly	
159	100								105					110			
160	cgc	tta	agc	aac	ata	act	tgc	tac	gaa	aca	atg	atg	gat	gcc	act	acg	385
161	Arg	Leu	Ser	Asn	Ile	Thr	Cys	Tyr	Glu	Thr	Met	Met	Asp	Ala	Thr	Thr	
162	115								120					125			
163	aag	ctt	caa	caa	gtc	atc	ctc	atc	gcc	gtg	gga	gtc	ttt	ctg	tcg	ctg	433
164	Lys	Leu	Gln	Gln	Val	Ile	Leu	Ile	Ala	Val	Gly	Val	Phe	Leu	Ser	Leu	
165	130								135					140			
166	gcf	gcf	ctg	gcf	ggg	ggc	tgt	ttc	ttc	ctg	gtg	ctg	aga	tac	aaa	ggc	481
167	Ala	Ala	Leu	Ala	Gly	Gly	Cys	Phe	Phe	Leu	Val	Leu	Arg	Tyr	Lys	Gly	
168	145								150					155			160
169	ctg	gtg	aaa	tac	tgg	ttt	cac	tct	ccg	cca	agc	atc	cca	tca	caa	atc	529
170	Leu	Val	Lys	Tyr	Trp	Phe	His	Ser	Pro	Pro	Ser	Ile	Pro	Ser	Gln	Ile	
171	165								170					175			
172	gaa	gag	tat	ctg	aag	gac	ccg	agc	cag	cct	atc	cta	gag	gcc	ctg	gac	577
173	Glu	Glu	Tyr	Leu	Lys	Asp	Pro	Ser	Gln	Pro	Ile	Leu	Glu	Ala	Leu	Asp	
174	180								185					190			
175	aag	gac	acg	tca	cca	aca	gat	gat	gcc	tgg	gac	ttg	gtg	tct	gtt	gtt	625
176	Lys	Asp	Thr	Ser	Pro	Thr	Asp	Asp	Ala	Trp	Asp	Leu	Val	Ser	Val	Val	
177	195								200					205			
178	gca	ttt	cca	gca	aag	gag	caa	gaa	gat	gtt	ccc	caa	agc	act	ttg	acc	673
179	Ala	Phe	Pro	Ala	Lys	Glu	Gln	Glu	Asp	Val	Pro	Gln	Ser	Thr	Leu	Thr	
180	210								215					220			
181	caa	aac	tct	ggf	gcf	gtc	tgc	tagcctgtgg	ggtaagggct	ctgagccgag						724	
182	Gln	Asn	Ser	Gly	Ala	Val	Cys										
183	225								230								
184	gaagctgctg	atgtccatgt	cagcacttta	tggaatccgg	tcctccattt	tcctgtcccc	784										
185	aaaaggcccg	tcagtgctg	tgaagatgta	acgggtctca	tgggggcgac	aagcttattg	844										
186	attttttct	tcaaactaag	agttttctaa	tcatacgcgt	tttttagaata	attctacaga	904										
187	tatgtccccg	aaagattaag	atttctctta	aacactaaaa	agacatgtaa	ttattttgtta	964										
188	gcaaatgggc	gtctggcacg	cctctgacac	tttttgcgtca	gcagccagga	cacgagggtcc	1024										
189	cctccttgc	gaagccccctc	gggcagacca	tgtcacctgt	cccagcctgc	cccaagaagg	1084										
190	gacattaagt	ggcccttctt	catatccaaa	cacctggctt	gaaatgtat	tagccctgtta	1144										
191	aatagttca	cagagattaa	gcctttttt	cccccaagtt	aggaataaaa	gactataatt	1204										
192	aacttttaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa			1244										
193	<210> SEQ ID NO 4																
194	<211> LENGTH: 231																

DATE: 03/24/1995  
TIME: 16:28:51

PAGE: 5

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/265,540

Input Set: I265540.RAW

195 <212> TYPE: PRT  
 196 <213> ORGANISM: primate  
 197 <400> SEQUENCE: 4  
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 200 Trp Phe Leu Ser Cys Trp Asn Val Thr Ile Gly Pro Pro Glu Ser Ile  
 201 20 25 30  
 202 Trp Val Thr Pro Gly Glu Ala Ser Leu Ile Ile Arg Phe Ser Ser Pro  
 203 35 40 45  
 204 Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe Gln Tyr Tyr Val His Xaa  
 205 50 55 60  
 206 Trp Glu Lys Ala Gly Ile Gln Lys Val Lys Gly Pro Phe Lys Ser Asn  
 207 65 70 75 80  
 208 Ser Ile Val Leu Asp Gly Leu Arg Pro Leu Arg Glu Tyr Cys Leu Gln  
 209 85 90 95  
 210 Val Lys Ala His Leu Phe Arg Thr Ser Cys Asn Thr Ser Arg Pro Gly  
 211 100 105 110  
 212 Arg Leu Ser Asn Ile Thr Cys Tyr Glu Thr Met Met Asp Ala Thr Thr  
 213 115 120 125  
 214 Lys Leu Gln Gln Val Ile Leu Ile Ala Val Gly Val Phe Leu Ser Leu  
 215 130 135 140  
 216 Ala Ala Leu Ala Gly Gly Cys Phe Phe Leu Val Leu Arg Tyr Lys Gly  
 217 145 150 155 160  
 218 Leu Val Lys Tyr Trp Phe His Ser Pro Pro Ser Ile Pro Ser Gln Ile  
 219 165 170 175  
 220 Glu Glu Tyr Leu Lys Asp Pro Ser Gln Pro Ile Leu Glu Ala Leu Asp  
 221 180 185 190  
 222 Lys Asp Thr Ser Pro Thr Asp Asp Ala Trp Asp Leu Val Ser Val Val  
 223 195 200 205  
 224 Ala Phe Pro Ala Lys Glu Gln Glu Asp Val Pro Gln Ser Thr Leu Thr  
 225 210 215 220  
 226 Gln Asn Ser Gly Ala Val Cys  
 227 225 230  
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 229 <211> LENGTH: 337  
 230 <212> TYPE: PRT  
 231 <213> ORGANISM: primate  
 232 <400> SEQUENCE: 5  
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 234 1 5 10 15  
 235 Ala Ala Ala Ala Ala Ala Pro Pro Asp Pro Leu Ser Gln Leu Pro Ala  
 236 20 25 30  
 237 Pro Gln His Pro Lys Ile Arg Leu Tyr Asn Ala Glu Gln Val Leu Ser  
 238 35 40 45  
 239 Trp Glu Pro Val Ala Leu Ser Asn Ser Thr Arg Pro Val Val Tyr Arg  
 240 50 55 60  
 241 Val Gln Phe Lys Tyr Thr Asp Ser Lys Trp Phe Thr Ala Asp Ile Met  
 242 65 70 75 80  
 243 Ser Ile Gly Val Asn Cys Thr Gln Ile Thr Ala Thr Glu Cys Asp Phe  
 244 85 90 95

VERIFICATION SUMMARY  
PATENT APPLICATION US/09/265,540DATE: 03/24/1999  
TIME: 16:28:51

Input Set: I265540.RAW

## Line ? Error/Warning

## Original Text

48 W "N" or "Xaa" used: Feature required  
85 W "N" or "Xaa" used: Feature required  
109 W "N" or "Xaa" used: Feature required  
111 W "N" or "Xaa" used: Feature required  
117 W "N" or "Xaa" used: Feature required  
119 W "N" or "Xaa" used: Feature required  
204 W "N" or "Xaa" used: Feature required

ggg atg gag atc ncc aaa nat ggc ttc cac c  
cttcatccct tnggtccnaa gttttctcat ctgtaatg  
Ile Xaa Lys Xaa Gly Phe His Leu Val Ile G  
Pro Gln Phe Glu Phe Leu Val Ala Tyr Trp X  
Val Lys Ala Ile Gly Xaa Tyr Ser Ala Phe S  
Xaa Val Gln Gly Glu Ala Ile Pro Leu Val L  
Phe Asp Val Pro Pro Asn Leu Gly Tyr Phe G

Application No.: 09/2855

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING  
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s)

1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

7. Other: \_\_\_\_\_

Applicant Must Provide:

An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216  
For CRF Submission Help, call (703) 308-4212  
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

COPY FOR [ ] File [ ] Applicant